

78939

From: Chan, Christina
Sent: Tuesday, October 29, 2002 2:05 PM
T: Fronda, Christian; STIC-Biotech/ChemLib
Subject: RE: Rush Search for Serial No. 09/819,930

Point of Contact
Susan Hanley
Technical Info. Specialist
CM1 6B05 Tel: 305-4053

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Fronda, Christian
Sent: Tuesday, October 29, 2002 1:24 PM
To: Chan, Christina
Subject: Rush Search for Serial No. 09/819,930
Importance: High

I am requesting a Rush Search for Serial No. 09/819,930 since it is an amended case now requiring a search.
Thank you.

Christian Fronda
Art Unit 1652
Mailbox CM1 10D01
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(703)305-1252

Please perform sequence search and interference search for Serial No. 09/819,930.

1. Please search SEQ ID No: 1 against nucleic acid commercial and interference databases including pending and issued.
2. Please search SEQ ID No: 2 against nucleic acid commercial and interference databases including pending and issued.
3. Please perform OLIGO Search for SEQ ID No: 2 against nucleic acid commercial and interference databases including pending and issued.

Please save on COMPUTER DISKETTES.

Please save results from interference data base search on different diskettes from the commercial and issued search results.

Thank you very much.

Christian Fronda
Art Unit 1652

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
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DRLink: _____
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Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

Dear Examiner,

The attached search was run with the most recently released version of Compugen's search software, GenCore 5. With this update, several changes have occurred in the results of FrameSearches (protein query sequence vs nucleic acid databases or nucleic acid query sequence vs protein databases).

In reference to FrameSearches:

- The output format has been improved so that it more closely resembles the format for standard search output.
- Calculation of Percent Similarity has been changed for FrameSearches. The new method of calculation is more similar to the method used in NCBI's BLAST algorithm. The same results are found in the same order using GenCore 5 and the previous version of GenCore, but Percent Similarities are lower in GenCore 5 results.
- The formula for % similarity calculation is:

$$100 * \frac{\text{matches} + \text{conservative substitutions}}{\text{alignment_length}}$$

where "matches" is the number of identical matches and "conservative substitutions" is the number of non-identical positive matches.

- GenCore 4.5 considers the match Thr vs GCT (Ala) to be a similarity since BLOSUM62 gives score of 0 to this match. It is marked by '...' in the alignment:

```
Qy      46 AspSerThrAspAla.Met..Gly 52
      |||||... ||| ... |||
Db      605 GATTCCGCTGCTGCTAATTTGGC 628
```

GenCore 5 requires a positive score to consider a non-identical match a similarity, therefore the same 'match' is not emphasized in the new alignment:

```
Qy      46 AspSerThrAspAla.Met..Gly 52
      ||||| ||| ... |||
Db      605 GATTCCGCTGCTGCTAATTTGGC 628
```

If you have any questions, please feel free to contact one of the searchers in Biotech/Chem Library.